

## **REMARKS**

Claims 15-29, 32-44 and 47-58 were pending in this application. Claims 16-20, 27, 33, 40-44, 47-51 and 55-58 have been withdrawn as directed to a non-elected invention. In this amendment claims 15-23, 27, 33, 35, 36, 42, 48-52, and 55-58 are canceled without prejudice. The remaining claims have been amended as indicated below. In particular claims 40 and 41 have been rewritten as claims to hybrid seed, rather than as a method for making hybrid seed. New claims 59-101 are added. All of claims 59-100 read on the elected species. New claim 101 depends from new claim 53, but is directed to the nucleotide sequence of SEQ ID NO:2 which is the portion of the sequence of SEQ ID No:1 which encodes the protein having the amino acid sequence of SEQ ID NO:3. Claims 24-26, 28, 29, 32, 34, 37-41, 43, 44, 47, 53, 54, and 59-101 are now in this case.

### **Amendments to the Specification**

The specification has been amended at page 1 as suggested by the Examiner to correct informalities and to update the status of the parent application. To facilitate amendment of page 1 a replacement page for page 1 of the specification is submitted herewith. The replacement page submitted does not include new matter.

The specification has also been amended to correct obvious typographic errors.

No new matter is added by the amendments to the specification.

### **Claim amendments**

All claims directed to DNA have been amended to recite "isolated DNA."

Claims directed to seeds have been amended to recite that the seed "comprises the DNA sequence" of the specified isolated DNA.

Claim 53 has been amended to depend from new claim 59. Claim 54 has been amended to delete reference to SEQ ID NO:2. New claim 101 has been added

which depends from claim 53 and recited that the isolated DNA has the DNA sequence of SEQ ID NO:2. Below Applicant requests examination of this claim along with those directed to nucleotide sequences encoding the protein having amino acid sequence of SEQ ID NO:3.

The broadest claims to transformants have been amended to recite that the transformant is a cell or tissue of a Brassica plant or is a Brassica plant or in other cases is a plant of the genus Brassica. The term "Brassica plant" is intended to have the same meaning as the "plant of the genus Brassica." Several claims have been amended to recite "*Brassica napus* plant," or "plant of the species *Brassica napus*." These amendments at least in part replace the term "rapeseed." The term rapeseed was originally used in the claims. The amendments to refer to *Brassica napus* was made for consistency of language with broader claims reciting Brassica. The term "*Brassica napus*" is intended to have the same meaning as "rapeseed."

Claims 24, 25, 28 and 32 are amended to depend from claim 53. All of claims 24-26, 28, 29, 32, 34, and 37-39 depend from claim 53. To improve clarity claim 25 was amended to delete reference to the vector. New claim 99 is now directed to a transformant comprising the vector of claim 24 which is a cell or tissue of a Brassica plant or is a Brassica plant. New claim 100 is directed to a transformant of claim 99 which is a cell or tissue of a *Brassica napus* plant or is a *Brassica napus* plant.

Claims 28 and 32 have been further amended to recite that the "promoter is positioned with respect to" the DNA coding sequence "to enable transcription thereof.

Claims 37 and 38 have been amended to delete reference to PPR sequences. Claim 38 has been further amended to improve clarity, to recite that the

transformant is *Brassica napus* and to recite that the GSL of the seeds is 30 micromole/g seed or less.

Claim 40 which was originally directed to a method has been rewritten to be directed to a hybrid plant seed having fertility restoration ability, produced by crossing a mother, which is a cytoplasmic male sterile line plant with a pollen parent, which is a fertility restoring line plant, which is a transformed plant of claim 26. The claim also recites that the seed "comprises a DNA sequence encoding the protein having the amino acid sequence of SEQ ID NO: 3," as recited in claim 53. Claims 41, 43, 44 and 47 depend from claim 40. Claims 41, 43 and 44 are also directed to hybrid seed and claim 47 is directed to plants and plant parts obtained by growing a seed of claim 40. These amendments are supported in original claims 40-44 and 47.

New claim 59 is a generic Markush-type claim directed to isolated DNA which encodes a protein involved in restoration of a cytoplasmic male sterile individual to fertility selected from a certain group of related DNAs encoding the amino acid sequence of SEQ ID NO:3, encoding amino acid sequences that exhibit 92% of higher homology to the amino acid sequence of SEQ ID NO:3, isolated DNAs having 95% or more sequence homology to the nucleic acid sequence from a DNA sequence encoding the amino acid of SEQ ID NO:3 or isolated DNAs which hybridized under defined stringent conditions to a DNA sequence encoding the amino acid sequence of SEQ ID NO:3.

Support for claims to DNA encoding amino acid sequence isolated DNA which encodes a protein having an amino acid sequence that is 92% or more homologous to the amino acid sequence of SEQ ID NO:3 is found in Example 15 in the paragraph bridging pages 78 and 79 where a comparison of the homology among the three amino acid sequences of the fertility restorer proteins of radish are noted to be 92.0%. Support for claims to an isolated DNA having 95% or

higher homology to a DNA sequence encoding a protein having the amino acid sequence of SEQ ID NO:3 is also found at the top of page 79.

Support for claims to isolated DNA which encodes a protein having an amino acid sequence wherein 1 to 20 amino acids are deleted, added and/or substituted in the amino acid sequences (3) an isolated DNA which encodes a protein having an amino acid sequence wherein 1 to 20 amino acids are deleted, added and/or substituted in the amino acid sequence of SEQ ID NO:3 is found in original claim 12, phrase (2), which refers to 1 or a plurality of amino acids deleted, added and/or substituted and on page 20 of the specification, lines 4-6, which further defined subsets of levels of variation, including from 1-20.

Applicants note that the sequence comparison in Example 15 shows more than 50 changes that can be made in the amino acid sequence of SEQ ID NO:3 while retaining functionality for restoration of male fertility. The term "a stringent condition" for hybridization is defined on page 20, lines 22-25 as "performing hybridization at 65 C in the presence of 0.7 to 1.0 M NaCl followed by washing the filter using 0.1 to 2X SSC solution (1 X SSC is composed of 150 mM sodium chloride and 15 mM sodium citrate) at 65 C."

Claims 60-72 depend from claim 59 and recite various aspects of the DNAs of claim 59. Again all of claims 60-72 are fully supported in the specification. Support for the recitations of amino acid sequences having 95% or higher and 97% or higher is found on page 16 of the specification, second paragraph, at lines 8-12. The paragraph refers to homology to the amino acid consensus sequences of SEQ ID NO:26-29, however, each of these consensus sequences encompasses the amino acid sequence of SEQ ID NO:3.

Claim 66 is directed to an isolated DNA encoding a protein in which 1 to 20 amino acids are deleted, added and/or substituted in the amino acid sequence of SEQ ID NO:3 and wherein the encoded protein conforms to the consensus sequences of SEQ ID NO:26 or SEQ ID NO: 27. This claim further limits the

deletions, additions and substitutions in the amino acid sequence of SEQ ID NO: 3 to only those that have been identified in the consensus sequences listed which were determined by a comparison of the amino acid sequence of SEQ ID NO: 3 with amino acid sequences of related proteins from radish. Applicants emphasize that this claim is not directed to a DNA encoding a protein having the listed SEQ ID NOS. so it is believed that no addition sequence searching is necessary for review of this claim.

New Claims 73 to 96 are directed to vectors comprising DNA sequences of the isolated DNA of claim 56, to transformants comprising these sequences as well as to transformants comprising the vector. These claims are supported in the specification and in as-filed claims.

New claims 97 is directed to a bacterial host cell comprising a vector of claim 73. A discussion of bacterial host cells is found in the specification at pages 31 and 32. The specific bacterial hosts of claim 98 are discussed and exemplified in the specification at page 33 and in the examples.

Claim 29 is directed to a method for maintaining a cytoplasmic male sterile line by using the transformant of claim 28. This method claim was not withdrawn from consideration. Because of this, Applicants have added new claim 84 which is directed to an analogous method where the transformant used in the method is that of claim 82.

None of the claim amendments represents the addition of new matter.

### **Claim Objections**

Claims 21, 22, 27, 40-44 and 47 were objected to for informalities. These claims have either been canceled or amended to correct informalities. The amendment to the claims obviates these objections.

### **Election of Species**

Applicants elected prosecution of SEQ ID NO:1 encoding SEQ ID NO:3. Claim 52 was objected to for reading on non-elected subject matter (non-elected SEQ ID NOS:17 and 19. Claim 54 was objected to for reading on non-elected SEQ ID NO:2.

Claim 53 is generically directed to an isolated DNA sequence encoding the amino acid sequence of SEQ ID NO:3. Claim 52 has been canceled. Dependent claim 54 has been amended to delete reference to the sequence of SEQ ID NO:2. The objections to claim 54 is obviated by this amendment

New claim 101 depends from claim 53 and recites that the sequence is that of SEQ ID NO:2:. The undersigned respectfully requests reconsideration of the exclusion of the sequence of SEQ ID NO:2 from consideration in this case. SEQ ID NO:2 is the coding sequence of SEQ ID NO:1. It is a subset of the sequence that has been searched. The undersigned appreciates that the Patent Office has legitimate reasons for limiting the amount of time that can be spent on sequence searching for a given application and that the search of the sequence of SEQ ID NO:1 was lengthy. However, because it is a contiguous portion of SEQ ID NO:, it seems that a search of SEQ ID NO:2 is inherent in the search of SEQ ID NO:1. It seems that the sequence search that has been conducted would encompass SEQ ID NO:2 as part of SEQ ID NO:1. If this is the case, then inclusion of SEQ ID NO:2 in this case would not represent an undue burden.

Claim 66 is directed to an isolated DNA which encodes a protein having an amino acid sequence wherein 1 to 20 amino acids are deleted, added and/or substituted in the amino acid sequence of SEQ ID NO:3 and wherein the protein has an amino acid sequence that conforms to the consensus sequences of SEQ ID NO:26, or SEQ ID NO:27. This claim reads on SEQ ID NO:1. Applicants have added reference to the consensus sequences to limit the types of deletions, addition and/or substitutions in the amino acid sequence encompassed by the

claim. The claim is not directed to an isolated DNA which encodes the consensus sequences themselves. As such it is believed that this claim properly reads on the elected species.

Claims 16-20, 33, 48-51 and 55-58 have been withdrawn as directed to a non-elected invention. All of these claims have been canceled.

### **Effective Filing Date**

The Office Action states that the effective filing date of the instant invention is 25 April 2001, the filing date of the earliest foreign priority application to disclose SEQ ID NO:1. SEQ ID NO:3 is alleged to be first disclosed in the foreign priority application filed 29 January 2002. The undersigned has only briefly reviewed the priority documents because all of the cited references appear to have effective dates as prior art before Applicants first priority date. Applicants preserve the right to dispute this interpretation of the content of the priority documents at a later time, if it is considered to be necessary.

### **The Rejections**

#### **35 U.S. C. 112, second paragraph rejections**

Claims 15, 21-23, 37, 39 and 52-54 are rejected under 35 USC 101 as directed to non-statutory subject matter. The claims have been amended to recite an "isolated" DNA which is believed to obviate the rejection.

Claims 37 and 39 are similarly rejected as directed to subject matter indistinguishable from naturally occurring seeds. These claims have been amended to recite that the seeds contain the DNA sequence of the specified isolated DNA. These amendments are believed to obviate the rejection.

Claims 21-23, 28-29, 32 and 34-39 are rejected under 35 USC 112, second paragraph as indefiniteness. The claims have been canceled or amended which is believed to obviate this rejection.

Claims 21-22 have been canceled. The language of new claim 59 and other new dependent claims is believed to recite proper Markush terminology and to be clear.

Claim 23 has been canceled and the term “homologue thereof” is no longer used in the claims.

Claim 28 is said to be unduly narrative and confusing. This claim has been amended to improve clarity.

Claims 32 and 35-38 are said to be indefinite in their recitation of promoter and DNA coding sequence where the relationship of the two sequences are not recited. Claims in which a promoter sequence is said to be combined with a coding sequence have been amended to recite that the promoter is positioned with respect to the coding sequence to enable transcription thereof.

#### 35 U.S.C. 112, first paragraph rejections

1. Claims 15, 21-26, 28-29, 32, 34-39 and 52 are rejected as failing to comply with the written description requirement. Claims 15, 21-23, 35, 36 and 52 have been cancelled. Claims 24-26, 32, 34, and 37-39 have been amended. It is believed that the amendment of the claims obviates this rejection.

The rejections refers to the claims as broadly drawn to those containing PPR motifs and to those which include multiple nucleotide additions, deletions and/or substitutions and to plant cells and plants transformed with them. It is alleged that the specification provides guidance only for the entire sequence of SEQ ID



NO:1 which encodes the protein of SEQ ID NO:3 and provides no guidance for sequence variants of SEQ ID NO:1.

Claim 24 is now directed to a vector comprising the DNA sequence of an isolated DNA of claim 53 which is an isolated DNA encoding a protein having the amino acid sequence of SEQ ID NO:3. Claim 25 is now directed to a transformant which comprising the DNA sequence of an isolated DNA of claim 53 and the transformant is recited to be a cell, tissue of a Brassica plant or a transformed Brassica plant. Claim 26 is similarly amended to be drawn to a transformed Brassica plant. Claim 28 has been amended to recite the introduction of the DNA sequence of an isolated DNA of claim 53\_and that the transformant is a plant cell or plant tissue of a Brassica plant or a transformed Brassica plant. Claim 29 depends from claim 28. Claims 32 and 34 now also recite the DNA sequence of an isolated DNA of claim 53. Claim 34 now recites a Brassica plant. Claims 37-39 depend from claim 25 which recites that the transformant is a cell, tissue of a Brassica plant or a Brassica plant.

Claims 24-26, 28, 29, 32, 34, and 37-39 are all believed to comply with the written description requirement in view of the reasoning presented in the rejection.

New claims 99-101 are also believed to comply with the written description requirement. Claim 97 is drawn to a transformant that contains a vector of claim 24 which is a cell or tissue of a Brassica plant or is a Brassica plant, while claim 98 is drawn to an analogous transformant which is a cell or tissue of a *Brassica napus* plant or is a *Brassica napus* plant. Claim 101 is directed to an isolated DNA encoding the protein having the amino acid sequence of SEQ ID NO: 3 which is SEQ ID NO:2. SEQ ID NO:2 is the coding sequence of SEQ ID NO:3 that is a part of SEQ ID NO:1. The use of this coding sequence for plant transformation is specifically exemplified in the specification.

The new claims 59-98 are also believed to comply with the written description requirement. All of claims 59-96 depend ultimately from claim 59. Claim 59 is drawn to a Markush group of related isolated DNA sequences. The isolated DNAs that are claimed include those that have some level of sequence variation with a DNA encoding the protein having the amino acid sequence of SEQ ID NO:3. Applicants note that the specification teaches the use of DNA encoding the protein having the amino acid sequence of SEQ ID NO:3. The specification further teaches two related amino acid sequences (SEQ ID NO:17, SEQ ID No:19) and a partial amino acid sequence SEQ ID NO.21 of proteins having the fertility restorer function of the protein of SEQ ID NO:3. The specification describes that proteins having amino acid sequences that have 92% or higher homology to the amino acid sequence of SEQ ID NO:3 retain the fertility restorer function. The specification describes that nucleotide sequences encoding the amino acid sequence of SEQ ID NO:3 and those encoding amino acid sequences that have 92 % or higher homology to SEQ ID NO:3 will function for transformation of plants, particular Brassica plants, for restoration of male fertility. The specification also describes nucleotide sequences having 95% homology to the disclosed genomic and coding sequences that will function for transformation of plants, particularly Brassica plants, for restoration of male fertility. Guidance is provided for the sequence variation encompassed by new claim 59.

With respect to transformants, the new claims recite that the transformants are cells or tissue of Brassica plants or are Brassica plants.

It is believed that all of the pending claims comply with the written description requirement.

To further demonstrate that the specification as a whole provides a sufficient written description of the isolated DNAs of claim 59. Applicants provide herewith a comparison of the three full amino acid sequences of the male fertility restorer proteins of this invention (Appendix A). The sequences were aligned and

compared as indicated and exhibited sequence identity of 91% with pairwise similarity of 94%. An analogous alignment and sequence comparison of the corresponding DNA encoding the three amino acid sequences is provided in Appendix B. The nucleotide sequences exhibit 95% identity. The nucleotide sequence of SEQ ID NO:2 is the coding sequence of SEQ ID NO:1 by which it encodes the protein of amino acid SEQ ID NO:3.

2. Claims 15, 21-26, 28-29, 32, 34-39 and 52 are rejected as being non-enabled by the specification. Claims 15, 21-23, 35, 36 and 52 have been cancelled. Claims 24-26, 28, 29, 32, 34, and 37-39 have been amended. It is believed that the amendment of the claims obviates this rejection.

The Office Action alleges that the specification is enabled only for claims limited to nucleic acids comprising the entire SEQ ID NO:1 or encoding the entire SEQ ID NO:3 and to Brassica and radish plants transformed therewith. As noted above the specification teaches three different, but related, proteins involved in the restoration of male fertility. The specification also teaches a portion of a fourth related protein. The specification compares the amino acid sequences of these proteins and teaches that sequences having 92% homology to SEQ ID NO:3 can retain function for restoration of male fertility. The specification teaches the use of all of the full coding sequences of these proteins for restoration of male fertility in plants, particularly Brassica plants.

All of claims 24-26, 28, 29, 32, 34 and 37-39 have been amended to recite a DNA having the sequence of an isolated DNA of claim 53 which is a nucleotide sequence which encodes the amino acid sequence of SEQ ID NO:3. All of these claims directed to transformants have been amended to recite that the transformant is a cell or tissue of a Brassica plant or is a Brassica plant. It is believed that these amendments obviate the rejection with respect to the listed claims.

New claims 99-101 are fully enabled by the specification. Claim 97 is drawn to a transformant that contains a vector of claim 24 which is a cell or tissue of a Brassica plant or is a Brassica plant, while claim 98 is drawn to an analogous transformant which is a cell or tissue of a *Brassica napus* plant or is a *Brassica napus* plant. Claim 101 is directed to an isolated DNA encoding the protein having the amino acid sequence of SEQ ID NO: 3 which is SEQ ID NO:2. SEQ ID NO:2 is the coding sequence of SEQ ID NO:3 that is a part of SEQ ID NO:1. The use of this coding sequence for plant transformation is specifically exemplified in the specification.

The new claims 59-98 are also believed to be fully enabled by the specification. All of claims 59-96 depend ultimately from claim 59. Claim 59 is drawn to a Markush group of related isolated DNA sequences. The isolated DNAs that are claimed include those that have some level of sequence variation with respect to DNAs encoding the amino acid sequence of SEQ ID NO:3.

Applicants note that the specification teaches the use of DNA encoding the protein having the amino acid sequence of SEQ ID NO:3. The specification further teaches two related amino acid sequences (SEQ ID NO:17, SEQ ID No:19) and a partial amino acid sequence SEQ ID NO:21 of proteins having the fertility restorer function of the protein of SEQ ID NO:3. The specification describes that proteins having amino acid sequences that have 92% or higher homology to the amino acid sequence of SEQ ID NO:3 retain the fertility restorer function. The specification describes that nucleotide sequences encoding the amino acid sequence of SEQ ID NO:3 and those encoding amino acid sequences that have 92% or higher homology to SEQ ID NO:3 will function for transformation of plants, particular Brassica plants, for restoration of male fertility. The specification also describes nucleotide sequences having 95% homology to the disclosed genomic and coding sequences that will function for transformation of plants, particularly Brassica plants, for restoration of male fertility. The specification provides for the sequence variation encompassed by new claim 59.

All of the pending claims are fully enabled by the specification. This rejection should be withdrawn.

### **Prior Art Rejections**

Claims 15, 21-22, 24-25, 28, 35-37 and 52 are rejected as anticipated by Cui et al. In this amendment claims 15, 21-22, 35, 36, and 52 have been canceled obviating this rejection with respect to those claims. Claims 24, 25, 28, and 37 have been retained and are amended. In each case, these claims ultimately depend from claim 53. Claim 53 has been found to be free of the cited prior art. Thus, all of amended claims 24, 25, 28 and 37 should be considered patentable over the cited reference.

Claims 15, 21-26, 28-29, 32, 34-39 and 52 are rejected as anticipated by Brown. Claims 15, 21-23, 35, 36, and 52 have been canceled. Claims 24, 25, 26, 28, 29, 32, 34, and 37-39 have been amended to ultimately depend from claim 53. Claim 53 has been found to be free of the cited prior art. Thus, all of amended claims 24, 25, 26, 28, 29, 32, 34, and 37-39 should be considered patentable over the cited reference.

It is believed that claim 52 was rejected as anticipated by Cui et al. or Brown because of a clerical error in the claim which referred to "an amino acid sequence of SEQ ID NO:3," which was interpreted to include a single amino acid sequence. The new claims do not have such a recitation.

It is believed that claims 21-22 (part 3) were rejected at least in part because it was interpreted that the claim was drawn to "DNA comprising any sequence which hybridizes under "a stringent condition" which includes conditions of low stringency." However, the term "a stringent condition" is defined in the specification on page 20, third full paragraph, as conditions where hybridization is

performed at 65 °C in the presence of 0.7-1.0 M NaCl followed by washing using 0.1 to 2 X SSC solution at 65 °C. It is believed that these hybridization conditions are not low stringency conditions.

New claims 59-98 all depend from claim 59 which recites a group of isolated DNAs which encode the protein having the amino acid sequence of SEQ ID NO:3 and isolated DNAs having some level of variation with respect to these DNAs. Claim 59 and its dependent claims are not anticipated by either of Cui et al or Brown. Neither of these references teach an isolated DNA encoding the protein having amino acid sequence SEQ ID NO:3 and neither of these references teaches any isolated DNA of related sequence as claimed in claim 59. Claims 15, 21-26, 28-29, 32, 34-39 and 52 are rejected as unpatentable over WO 97/49831 in view of Moloney et al. and in further view of Delourme et al. Claims 15, 21-23, 35, 36, and 52 have been canceled. Claims 24, 25, 26, 28, 29, 32, 34, and 37-39 have been amended to ultimately depend from claim 53. The isolated DNA of claim 53 which is isolated DNA that encodes the amino acid sequence of SEQ ID NO:3 has been found to be free of the prior art of record. It is thus believed that all of the listed pending amended claims are patentable over the combination of references in this rejection. This rejection should be withdrawn.

New claims 99-101 all ultimately depend from claim 53 and are also believed to be patentable over the cited combination of references.

New claims all depend from claim 59 which recites a group of isolated DNAs which encode the protein having the amino acid sequence of SEQ ID NO:3 and isolated DNAs having some level of sequence variation with respect to these DNAs.

None of the references cited in this rejection teaches or suggests an isolated DNA encoding the protein having amino acid sequence SEQ ID NO:3 and none

of the cited references teaches or suggests any isolated DNA of related sequence as claimed in the parts of claim 59.

There is nothing on the record to show that any of the cited references teach or suggest an amino acid sequence having 92% homology to the amino acid sequence of SEQ ID NO:3 and nothing to teach or suggest any isolated DNA encoding such amino acid sequences. There is nothing on the record to show that any of the cited references teach or suggest isolated DNAs which have 95% or higher homology to a DNA sequence encoding the amino acid sequence of SEQ ID NO:3. There is nothing on the record to show that any of the cited references teach or suggest amino acid variants of SEQ ID NO:3 which have 1-20 amino acid additions, deletions or substitutions of the amino acid sequence of SEQ ID No:3 or isolated DNAs encoding such protein variants. There is nothing on the record to show that any of the cited references teach or suggest isolated DNAs which hybridized under the conditions listed in claim 59, which are not low stringency conditions, to a DNA which encodes the amino acid sequence of SEQ ID NO:3. Claim 72 is drawn to isolated DNA sequences which hybridize under what is believed to be clearly high stringency conditions (0.1 X SSC wash at 65°C) to DNA sequences which encode the amino acid sequence of SEQ ID NO:3. There is nothing on the record to show that any of the cited references teach or suggest an isolated DNA as claimed in claim 72.

In view of all of the foregoing, the pending claims should be considered patentable over the prior art of record herein.

### **Conclusion**

In view of the amendment of the claims and the arguments presented, it is believed that all of the remaining claims are patentable and should be allowable. Passage to issuance is respectfully requested. This response requires the payment of excess claim fees for two dependent claims. It is believed that fees are due in the amount of \$100 (large entity) for this submission. The Patent

Office is authorized to deduct the required fees for excess claims, and any other fees required for submission of this response, from Deposit Account No.

07-1969. It is believed that no extension of time is required.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Sally A. Sullivan", with a long, sweeping horizontal line extending to the right.

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